

Figure 2A

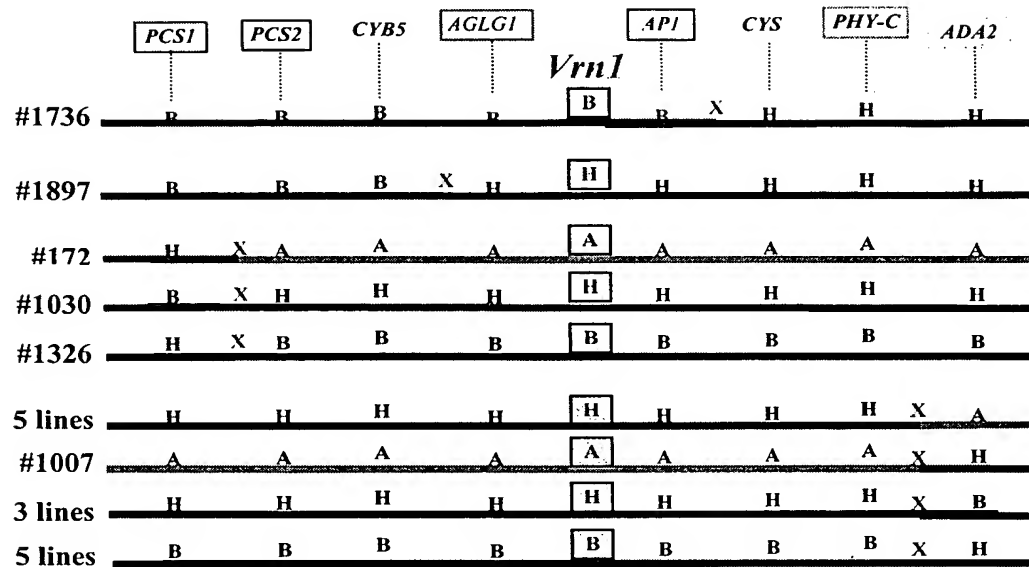


Figure 2B

F ₂ family	G2528	G1777	AA		AB		BB	
			N	D	N	D	N	D
#1736	0 D	45 D	10	-5/+1	16	-5/0	10	-5/+1
#1897	0 D	60 D	7	35/40	22	-5/0	8	-5/0

Figure 3

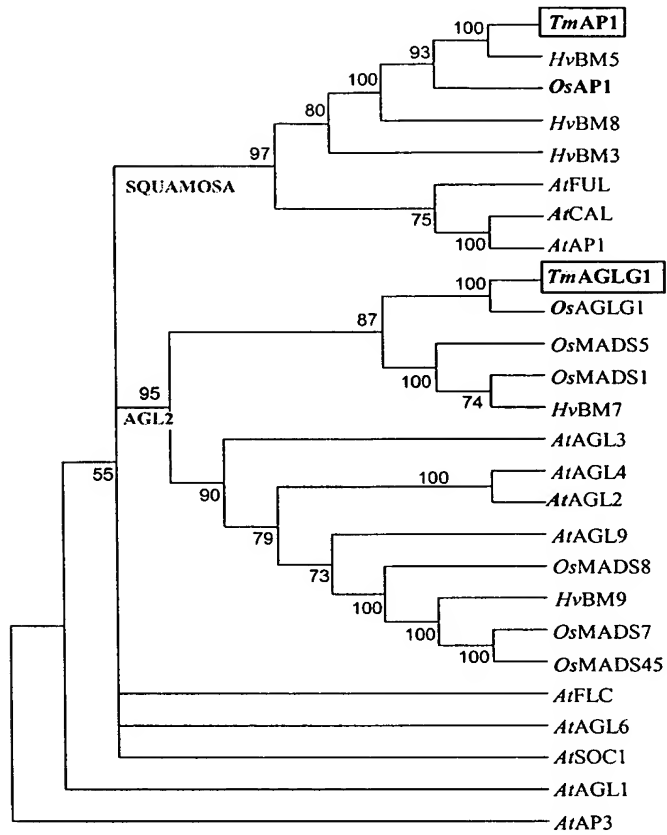
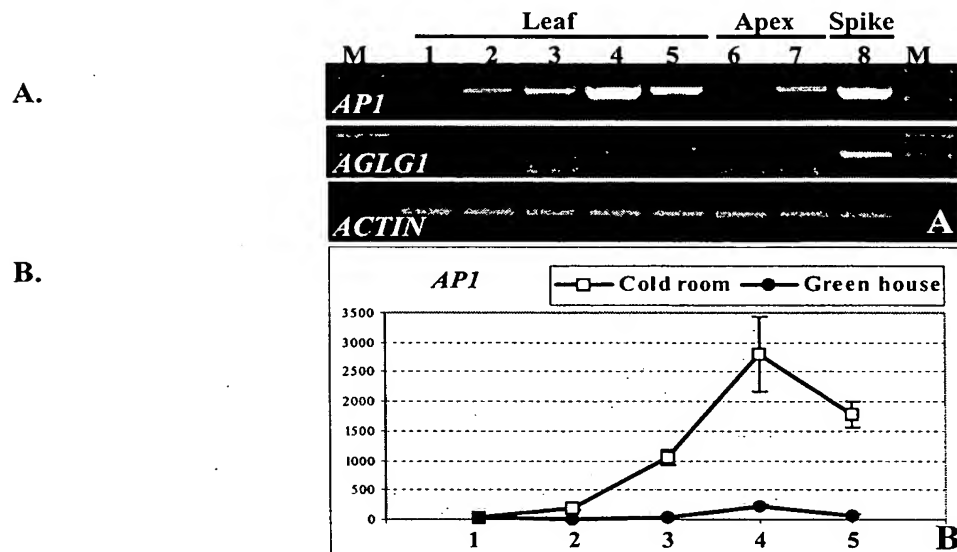


Figure 4



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Figure 5

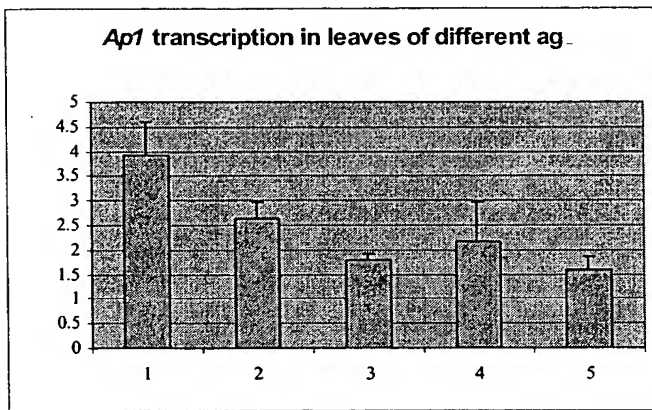


Figure 6

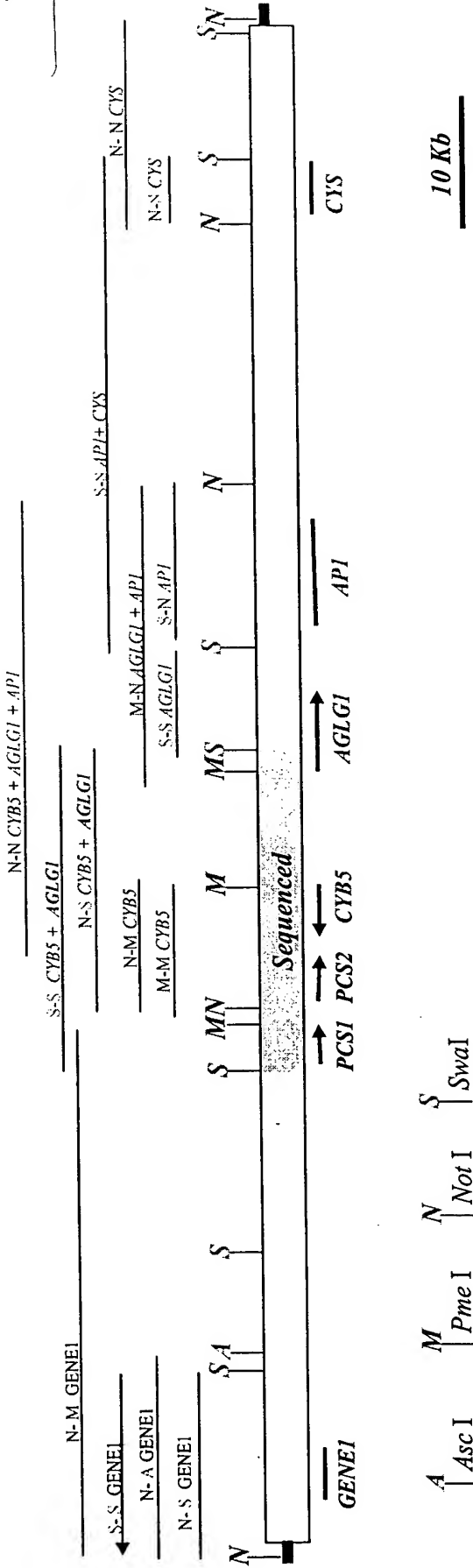


Figure 8

- A. G2528 (*Vrn1*) = DV92 (*vrn1*)
MGRGKVQLKRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVGLIIFSTKGKLYEFSTESCMDKILERYER
YSYAEKVLVSSSESEIQGNWCHEYRKLKAKVETIQKCQKHLMGEDLESNLKELQQLEQQLESSLKHIRSR
KNQLMHESISELQKKERSLQEENKVLQKELVEKQKAHAAQQDQTQPQTSSSSSFMLRDAPPAANTSHP
AAAGERAEDA AVQPAPPTGLPPWMVSHING* (SEQ ID NO: 7)
- B. G1777 (*vrn1*) = G3116(*vrn1*)
MGRGKVQLKRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVGLIIFSTKGKLYEFSTESCMDKILERYER
YSYAEKVLVSSSESEIQGNWCHEYRKLKAKVETIQKCQKHLMGEDLESNLKELQQLEQQLESSLKHIRSR
KNQLMHGSISELQKKERSLQEENKVLQKELVEKQKAHAAQQDQTQPQTSSSSSFMLRDAPPAANTSHP
AAAGERAEDA AVQPAPPTGLPPWMVSHING* (SEQ ID NO: 8)

Figure 9A

G2528 1 ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC
DV92 1 ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC
G1777 1 ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC
G3116 1 ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC

G2528 61 ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTTCATTCCAGAAATACG
DV92 61 ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTTCATTCCAGAAATACG
G1777 61 ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTTCATTCCAGAAATACG
G3116 61 ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTTCATTCCAGAAATACG

G2528 121 CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGAGCGCACTGCAC
DV92 121 CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGAGCGCACTGCAC
G1777 121 CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGAGCGCACTGCAC
G3116 121 CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGAGCGCACTGCAC

G2528 181 TGCACAGCAACGCTTCATGTCAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC
DV92 181 TGCACAGCAACGCTTCATGTCAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC
G1777 181 TGCACAGCAACGCTTCATGTCAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC
G3116 181 TGCACAGCAACGCTTCATGTCAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC

G2528 241 GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCTGCCCGCAGCCG
DV92 241 GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCTGCCCGCAGCCG
G1777 241 GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCTGCCCGCAGCCG
G3116 241 GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCTGCCCGCAGCCG

G2528 301 ACCTCTCCCCAACGGGACAAGCGAGACGGCCCAAACGAGCAAGGAAAGCAGCCTCCTA
DV92 301 ACCTCTCCCCAACGGGACAAGCGAGACGGCCCAAACGAGCAAGGAAAGCAGCCTCCTA
G1777 301 ACCTCTCCCCAACGGGACAAGCGAGACGGCCCAAACGAGCAAGGAAAGCAGCCTCCTA
G3116 301 ACCTCTCCCCAACGGGACAAGCGAGACGGCCCAAACGAGCAAGGAAAGCAGCCTCCTA

G2528 361 CTGTGGCAGCCCGCCCCACGACCGTCATCTCCCTTCCATTTCATTTCCCTGGACGGA
DV92 360 CTGTGGCAGCCCGCCCCACGACCGTCATCTCCCTTCCATTTCATTTCCCTGGACGGA
G1777 360 CTGTGGCAGCCCGCCCCACGACCGTCATCTCCCTTCCATTTCATTTCCCTGGACGGA
G3116 360 CTGTGGCAGCCCGCCCCACGACCGTCATCTCCCTTCCATTTCATTTCCCTGGACGGA

G2528 421 CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCTCTTTTCGTCCCCCGCC
DV92 420 CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCTCTTTTCGTCCCCCGCC
G1777 420 CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCTCTTTTCGTCCCCCGCC
G3116 420 CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCTCTTTTCGTCCCCCGCC

G2528 481 GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAAATGCTAAAGGAAAAAACTCCGCTC
DV92 480 GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAAATGCTAAAGGAAAAAACTCCGCTC
G1777 480 GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAAATGCTAAAGGAAAAAACTCCGCTC
G3116 480 GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAAATGCTAAAGGAAAAAACTCCGCTC

G2528 541 TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTTCTGCTCGT
DV92 540 TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTTCTGCTCGT
G1777 540 TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTTCTGCTCGT
G3116 540 TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTTCTGCTCGT

G2528 601 TTTTGTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAAATGATTGGGGAAAGCAAAATCGG
DV92 600 TTTTGTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAAATGATTGGGGAAAGCAAAATCGG
G1777 600 TTTTGTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAAATGATTGGGGAAAGCAAAATCGG
G3116 600 TTTTGTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAAATGATTGGGGAAAGCAAAATCGG

G2528 661 GAGATTCGCACGTACGATCGTTTCGACACGTCGACGCCCGCGGGCCCGTGGTGGGGCATC
DV92 660 GAGATTCGCACGTACGATCGTTTCGACACGTCGACGCCCGCGGGCCCGTGGTGGGGCATC
G1777 660 GAGATTCGCACGTACGATCGTTTCGACACGTCGACGCCCGCGGGCCCGTGGTGGGGCATC
G3116 660 GAGATTCGCACGTACGATCGTTTCGACACGTCGACGCCCGCGGGCCCGTGGTGGGGCATC

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Figure 9B

G2528	721	GTGTGGCTGCAGGACCGCGGGGCCCCCGGGGCGGGCCGAGCAATGGGTGCTCGACAGC
DV92	720	GTGTGGCTGCAGGACCGCGGGGCCCCCGGGGCGGGCCGAGCAATGGGTGCTCGACAGC
G1777	720	GTGTGGCTGCAGGACCGCGGGGCCCCCGGGGCGGGCCGAGCAATGGGTGCTCGACAGC
G3116	720	GTGTGGCTGCAGGACCGCGGGGCCCCCGGGGCGGGCCGAGCAATGGGTGCTCGACAGC
G2528	781	GGCTATGCTCCAGACCAGCCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
DV92	780	GGCTATGCTCCAGACCAGCCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
G1777	780	GGCTATGCTCCAGACCAGCCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
G3116	780	GGCTATGCTCCAGACCAGCCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
G2528	841	ACCC-----TCGTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
DV92	840	ACCCCTCCCCCCTGCCGGAACCCCTCGTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
G1777	840	ACCCCTCCCCCCTGCCGGAACCCCTCGTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
G3116	840	ACCCCTCCCCCCTGCCGGAACCCCTCGTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
G2528	881	TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
DV92	900	TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
G1777	900	TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
G3116	900	TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
G2528	941	CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTGGAGGGTAGGGGCGTAGGGTTGGCCCG
DV92	960	CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTGGAGGGTAGGGGCGTAGGGTTGGCCCG
G1777	960	CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTGGAGGGTAGGGGCGTAGGGTTGGCCCG
G3116	960	CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTGGAGGGTAGGGGCGTAGGGTTGGCCCG
G2528	1001	GTTCTCGAGCGGAGATC Start codon (SEQ ID NO: 9)
DV92	1020	GTTCTCGAGCGGAGATC Start codon (SEQ ID NO: 10)
G1777	1020	GTTCTCGAGCGGAGATC Start codon (SEQ ID NO: 11)
G3116	1020	GTTCTCGAGCGGAGATC Start codon (SEQ ID NO: 12)

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Figure 10



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Figure 11

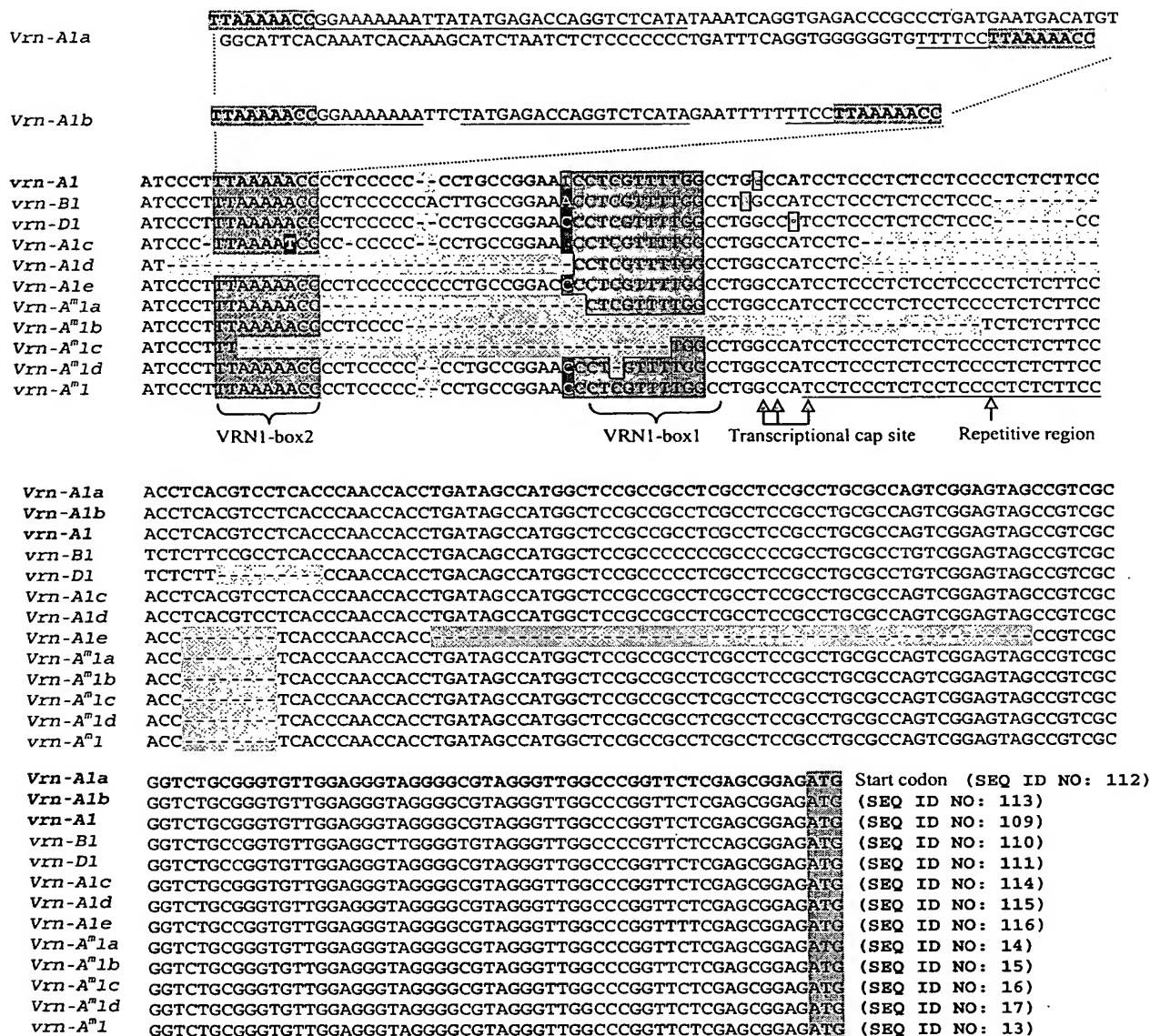


Figure 12

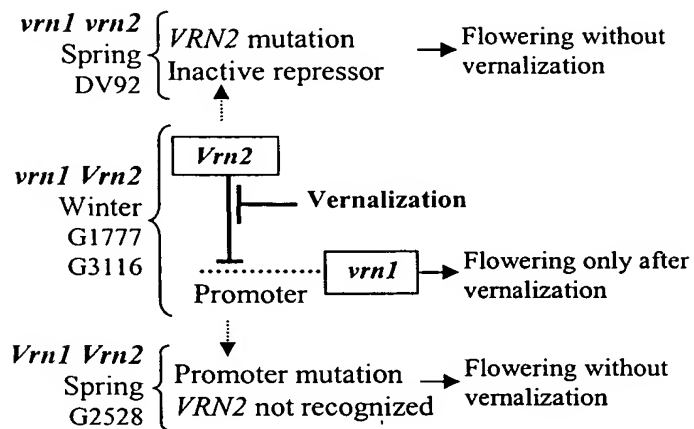


FIGURE 13

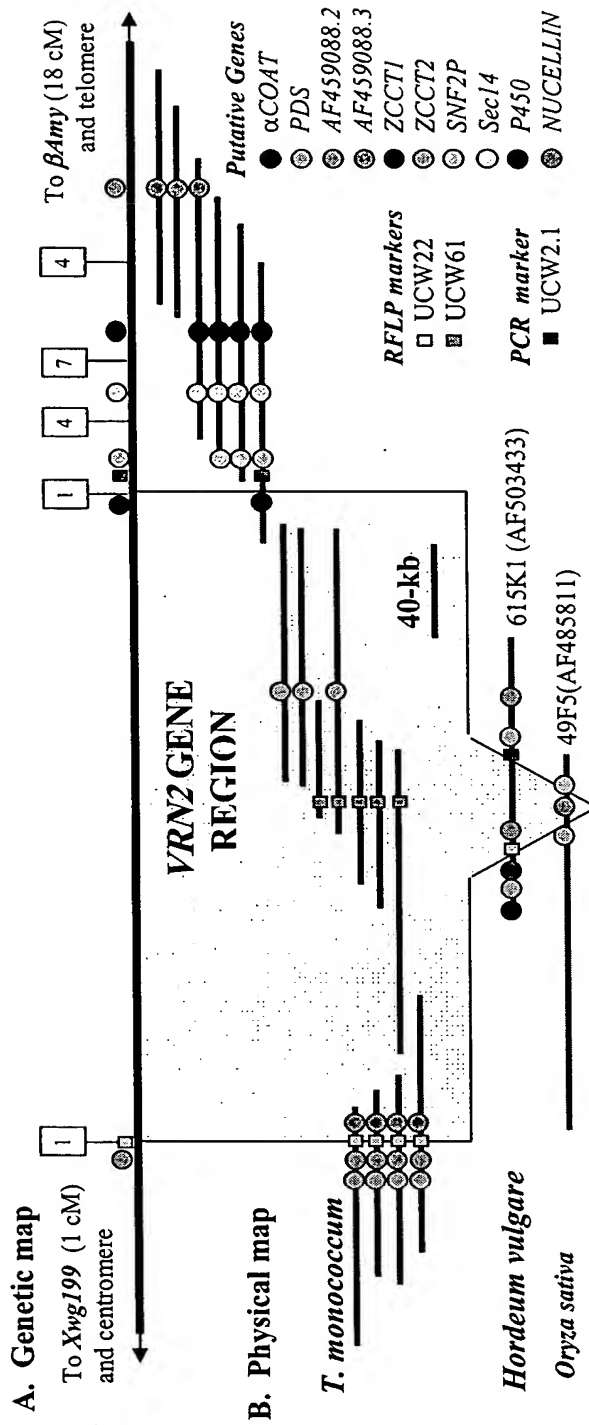
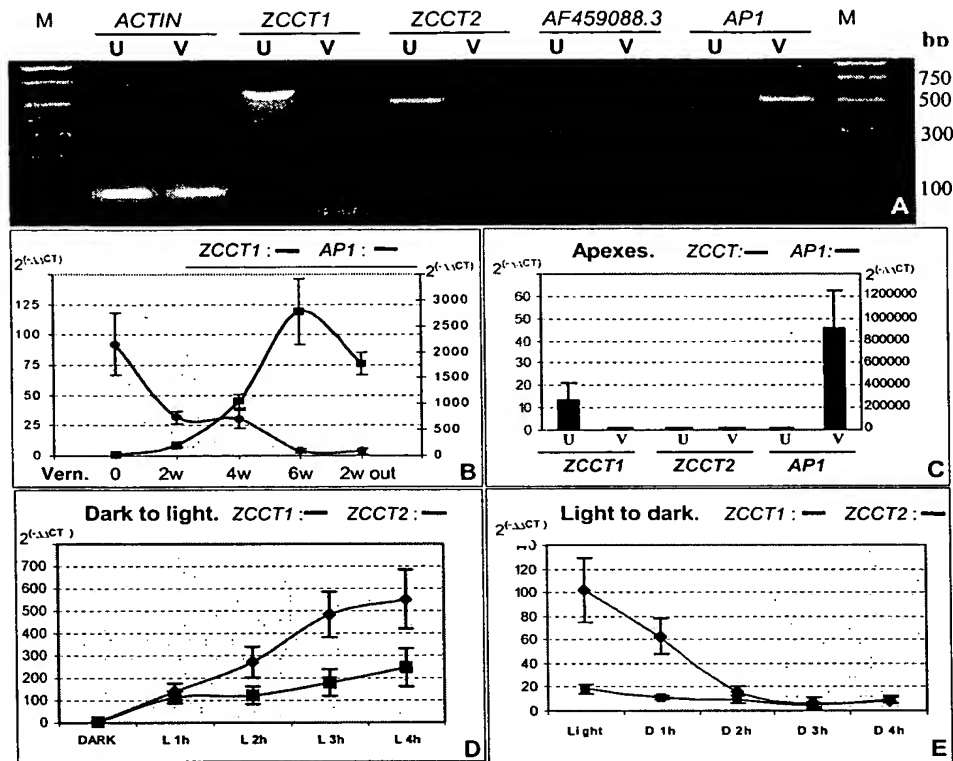


FIGURE 14



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FIGURE 15A



Transgenic Jagger cDNAs

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FIGURE 15B

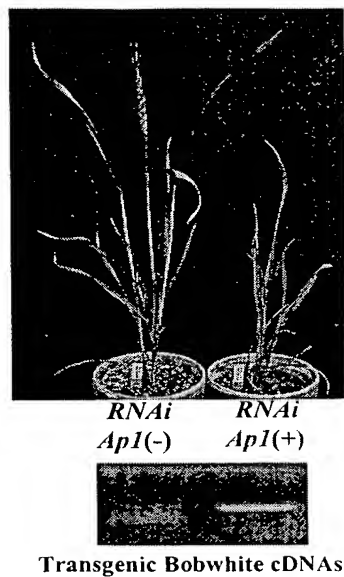


FIGURE 15C



FIGURE 16

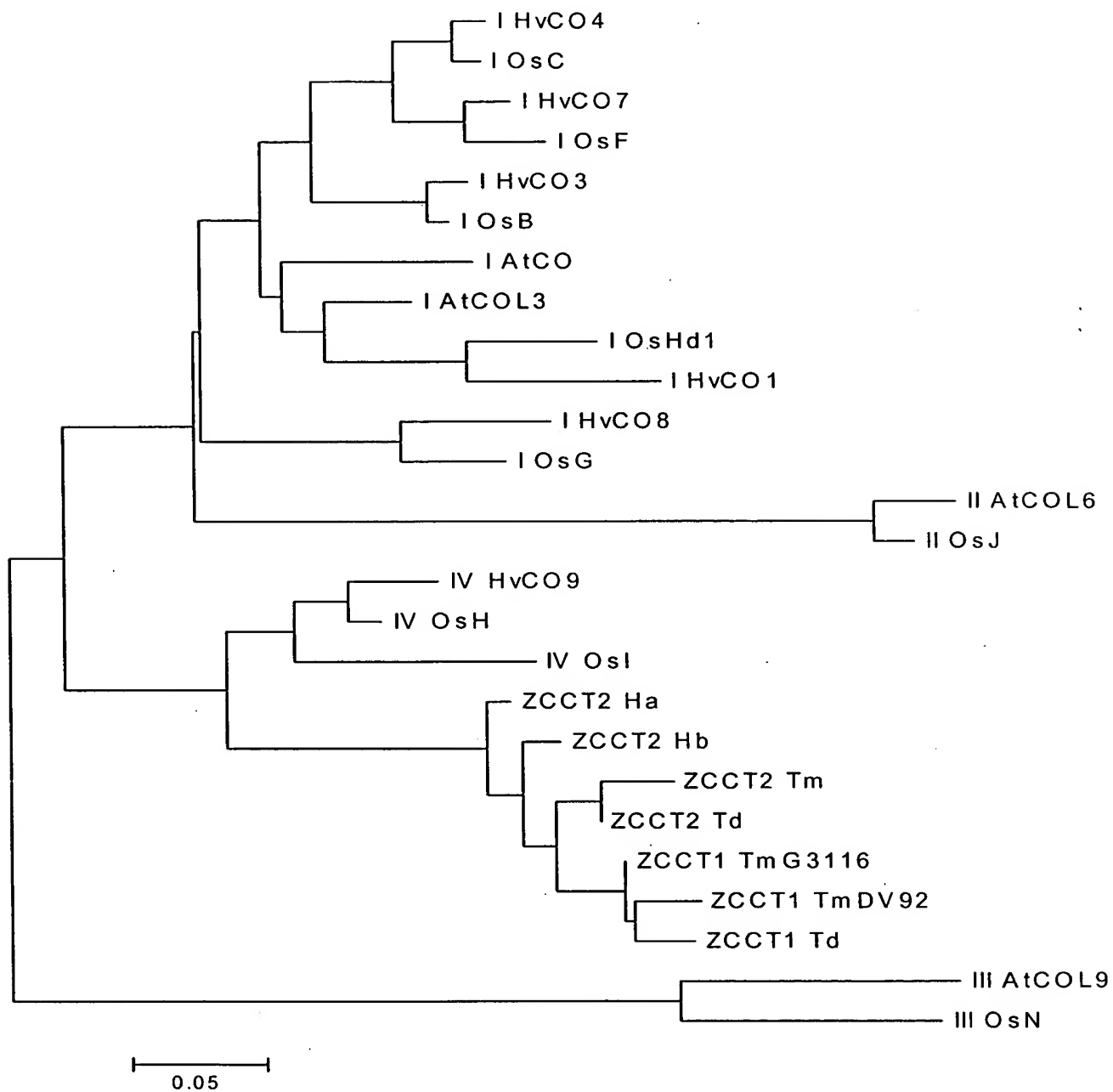


FIGURE 17

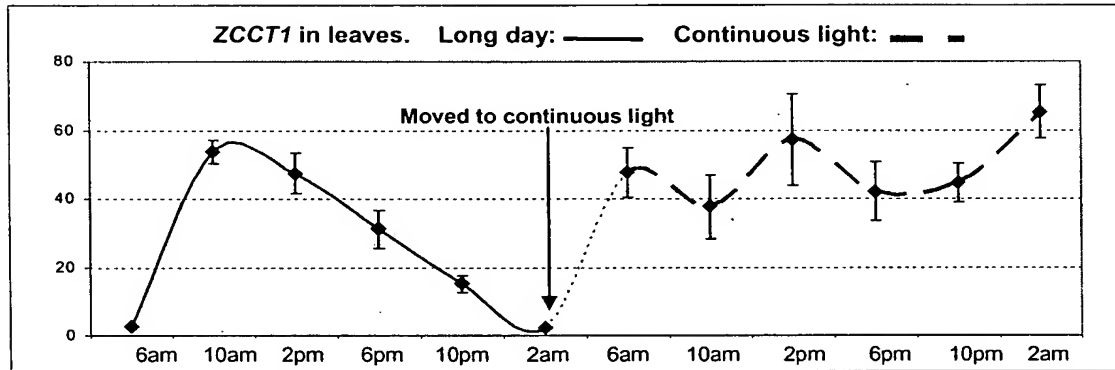


FIGURE 18

A

ZCCT1_TmDV92	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 117)
ZCCT1_TmG3116	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 118)
ZCCT1_Td	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 119)
ZCCT2_Tm	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 120)
ZCCT2_Td	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 121)
ZCCT2_Hb (Fan)	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 122)
ZCCT2_Ha	ERAAKVMRYREKRKRYYDKQIRYESRKAYAEIRPVNGRFVKV	(SEQ ID NO: 123)
OsI	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 124)
HvCO9	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 125)
OsH	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 126)
AtCO	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 127)
OsHd1	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 128)
HvCO1	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 129)
HvCO3	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 130)
OsB	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 131)
HvCO4	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 132)
OsC	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 133)
AtCOL3	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 134)
HvCO7	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 135)
OsF	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 136)
HvCO8	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 137)
OsG	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 138)
AtCOL6	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 139)
OsJ	EREAKLMRYEKRKRYYEKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 140)
AtCOL9	TRNNAMRYEKKKKRYYDKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 141)
OsN	SRDNALTRYEKKKKRYYDKQIRYASRKAYAEIRPVNGRFVKV	(SEQ ID NO: 142)

Tm=*T. monococcum*, Td=*T. dicoccoides* A genome, Hv=*Hordeum vulgare*, Os=*O. sativa*.

FIGURE 18

B

ZCCT1_Td_A MSMSGGLCGANNCPRMLVSPIH~~HHHH~~QEHQL Hx₃H position not certain
(SEQ ID NO: 143)
ZCCT1_DV92 MSMSGGLCGANNCPRMLVSPIH~~HHHHH~~QEHQL Hx₃H position not certain
(SEQ ID NO: 144)
ZCCT1_G3116 MSMSGGLCGANNCPRMLVSPIH~~HHHHH~~QEHQL Hx₃H position not certain
(SEQ ID NO: 145)
ZCCT-Hb (Fan) MSMA~~CGLCGAS~~NC~~PYHMMSPV~~~~HHHHH~~QEHRL Hx₃H position not certain
(SEQ ID NO: 146)
ZCCT-Ha MSMSGGLCGASNC~~YHMMSPV~~~~HHHHH~~QEH~~L~~ Hx₃H position not certain
(SEQ ID NO: 147)
ZCCT2_Td_B ~~MSMSGGLCGAS~~NC~~PHHMM~~SP~~VLOHCHHH~~QEHRL Hx₃H position not certain
(SEQ ID NO: 148)
ZCCT2_DV92 ~~MSMSGGLCGAS~~DC~~PHHMM~~SP~~VLOHCHHH~~QEHRL Hx₃H position not certain
(SEQ ID NO: 149)
ZCCT2_Td_A ~~MSMSGGLCGAS~~DC~~PHHMM~~SP~~VLOHCHHH~~QEHRL Hx₃H position not certain
(SEQ ID NO: 150)

CO-LIKE GROUP IV (Yellow highlight: similar ZCCT)

OsI (SEQ ID NO: 151) MGMANEESP~~NYQVKKG~~RIPPRSSLIYPFMSMGPAAGEG~~CGLCGADGGGCCSR~~HRHD
OsH (SEQ ID NO: 152) MSAASGAAC~~GVCGGGVGECC~~LLHQRG

CO-LIKE Group I, II, III

HvCO1 (SEQ ID NO: 153) MNCVSN~~GT~~VYEEAVGREGRWARL~~GDG~~CTVPSVVYCRADSAYL~~CGAS~~DA
HvCO3 (SEQ ID NO: 154) MIKAEPDLRGQLRGSAGVGGMQLQQRCDSCRSAPCAFYCRADSAAL~~CAAC~~DA
HvCO4 (SEQ ID NO: 155) MEGEEKPVVGGAYWVGARACDSCATEAARLFCRADA~~AF~~LCAG~~DA~~
(SEQ ID NO: 156) RAHSGSRHARVWL~~CEV~~CEHAPAAVTCKADA~~AV~~LCAS~~DA~~
OsJ (SEQ ID NO: 157) MASAAAAATGAALGARTARACDGMRRRRARWHCPADDAFL~~QA~~DA
OsN (SEQ ID NO: 158) MDALCDFCREQ~~RS~~SMVYCRSDAASL~~CL~~SCDRNVHSANALSRRHTRTLL~~CDR~~GVGQ
(SEQ ID NO: 159) PAAVRCLEENTSL~~CONC~~DWNGHGAASSAAGHKQTIN~~GYSG~~P